tween PTA_1 and PTA_3, and 0.97 between PTA_2 and PTA_3 for US daughters; corresponding correlations were 0.90, 0.88, and 0.98 for Canadian daughters. Correlations between PTA_2 - PTA_1 and EBV_2 - EBV_1 were 0.63 for 599 bulls with ≥20 daughters, 0.82 for 311 bulls with ≥100 daughters, and 0.89 for bulls with ≥500 daughters in both countries; corresponding correlations were 0.54, 0.76, and 0.85 for differences between third- and first-parity sire evaluations. Corresponding correlations for differences between third- and second-parity sire evaluations were considerably lower at 0.14, 0.27, and 0.52, probably because differences between second- and third-parity evaluations were small. Differences in maturity rate of bull daughters were reasonably consistent across countries. Modeling genetic evaluations to account for those differences would increase accuracy for bulls with daughters that deviate substantially from population mean.

Key Words: Maturity Rate, Milk Yield, Parity

M21 Factors affecting heifer fertility in US Holsteins. M. Kuhn* and J. Hutchison, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Heifer breedings from January 2003 to October 2004 were used to investigate factors affecting heifer fertility. There were 331,469 breedings on 220,624 Holstein heifers. Only artificial inseminations were analyzed. Age at breeding was required to be between 8 months and 3 years. Only 0.33% of breedings occurred at ages > 2.5 years; 98.2% of all breedings were at ages < 2 years. The dependent variable for analysis was 0 (no conception) or 1 (conception). A heifer's last recorded service was considered a success. Breedings were included only if there was at least 2 months for a repeated service to be reported. The linear model for analysis included the fixed effects of herd, year, month, and age-at-breeding, and the covariates of parent average predicted breeding value for milk, SCS, and daughter pregnancy rate (DPR). The overall arithmetic mean conception rate was 0.64 with a 0.48 standard deviation. The only factors that did not have a significant effect on heifer conception were parent average breeding values for milk and SCS. Year accounted for the most variation in heifer conception rate. Year 2004 had a 6% higher conception rate than 2003. This may be a realistic difference between years or it may indicate that additional editing needs to be investigated. Perhaps 2 months is not an adequate amount of time to wait for a reported service in the case of heifers. Month of breeding accounted for the second largest amount of variation with January and February having the poorest conception rates and September and October having the best. Parent average breeding value for DPR accounted for the third most variation with conception rate increasing as DPR increased. Selection on DPR will improve fertility in heifers as well. Age at breeding accounted for more variation than herd; conception rates increased with age. Further research will investigate appropriate edits for heifer breedings and also compare linear model results to results from logistic and probit models.

Key Words: Heifer Bbreedings, Daughter Pregnancy Rate, Fertility

M22 Effectiveness of estimating individual herd heritabilities using regression techniques. C. D. Dechow*[1] and H. D. Norman[2], [1]*Penn State University*, *University Park*, [2]*Animal Improvement Programs Laboratory*, *Beltsville, MD*.

The objectives of this study were to estimate heritabilities for individual herds using regression techniques and determine if incorporating individual herd heritability would increase accuracy of genetic evaluations. First lactation mature equivalent milk (MEM) was obtained from 64,350 first lactation cows in 45 herds with 500 or more cows. Individual herd heritability was estimated using REML (h^2_{RML}), daughter-dam regression (h^2_{DD}), and daughter-sire estimated breeding value regression (h^2_{DS}). Regression coefficients were estimated for each herd with the MIXED procedure of SAS. The model included fixed year-season and age at calving effects, either dam MEM (DM) or sire estimated breeding value (SEBV) as a random covariable, and random error. Animal models were also used to estimate heritability for each herd with ASREML. Heritability from daughter-dam regression was twice the regression of MEM on DM. Twice the regression of MEM on SEBV was multiplied by genetic variance of the US Holstein population and divided by herd phenotypic variance to estimate h^2_{DS}. Sex averaged heritability (h^2_{SA}) was the mean of h^2_{DD} and h^2_{DS}. Heritability estimates were constrained to range from 0.25 to 0.35 and were used to standardize records to a constant genetic variance across herds. Estimated breeding values (EBV) were generated with the adjusted records, which were weighted by the ratio of base error variance to herd error variance. Average individual herd heritability estimates ranged from 0.28 for h^2_{RML} to 0.31 for h^2_{DD}. Correlations of h^2_{RML} with h^2_{DD}, h^2_{DS}, and h^2_{SA} were 0.53, 0.42 and 0.61, respectively. Correlations among sire EBV generated with the adjusted records and official sire PTAM from November 2004 national genetic evaluations ranged from 0.007 to 0.012 higher than the correlation when using non-adjusted records. Correlations between yield deviations and parent averages were lower (range -0.026 to -0.002) after adjustment for heritability, except adjustments for h^2_{DD} (0.006 higher). Individual herd heritability estimates may improve accuracy of national genetic evaluations, or help identify progeny test herds with poor parent identification.

Key Words: Heritability, Yield, Accuracy

M23 Accounting for heterogeneous variances in multi-trait evaluation of Jersey type traits. N. Gengler[1], G. Wiggans[2], L. Thornton*[2], J. Wright[2], and T. Druet[1], [1]*National Fund for Scientific Research, B-1000*, *Brussels, Belgium*, [2]*Animal Improvement Programs Laboratory*, *Beltsville, MD*.

The multi-trait genetic evaluation system for type traits was modified to estimate adjustments for heterogeneous variance (HV) simultaneously with estimated breeding values (EBV) for final score and 14 linear traits. Heterogeneity, estimated for transformed traits, was regressed within parity toward the population variance means by fitting a model with fixed effects of mean final score for herd, size of contemporary group, appraisal month, and appraisal year-season and a random effect for interaction between herd and appraisal date. Method R was used to estimate variances for the heterogeneity model in each EBV iteration. Data was from the 766,725 appraisals included in the official November 2004 evaluation. Parent averages were calculated from evaluations with recent appraisals removed. Annual trends for cow EBV were lower with HV adjustment than for unadjusted EBV for all traits. The SD of Mendelian sampling (evaluation minus mean of parent evaluations) declined less over time for HV adjusted than for unadjusted evaluations. The slope at year 2000 of Mendelian-sampling SD from HV adjusted evaluations was only 22% for udder depth to 48% for teat length of the slope of that for unadjusted evaluations. This adjustment for HV was implemented in May 2001 and should make selection decisions more accurate by using these proposed integrated HV adjustments.

Key Words: Heterogeneous Variance Adjustment, Type Evaluation

M24 Comparison of lifetime relative net income with and without adjustment for opportunity cost. E. Yook, R. Pearson*, and B. Cassell, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

The purpose of this study was to compare relationship of lifetime relative net income (RNI) and RNI adjusted for opportunity cost (RNIOC) for 6 herd life opportunity lengths based on 305d or complete milk records. RNI and RNIOC were calculated on 70,167 cows born in 1988, 1990, and 1992 from IN, FL, NC, TX, VA, and VT using the milk pricing assumed in Net Merit calculations and based on either 305d or complete lactation records for periods of herd life from 5 to 10 years. Opportunity cost was estimated for each cow by multiplying her total days of productive life in herd times the mean herd RNI divided by mean herd days of productive life. RNIOC for 10yr herd life opportunity estimated from complete lactations was regressed on 5, 6, 7, 8, and 9yr herd life opportunity (β= 1.2, 1.13, 1.07, 1.04, 1.01; R^2 =.74, .87, .94, .98, and .99). Similarly regressions predicting RNI for 10 yr herd life opportunity were run (β = 1.45, 1.26, 1.14, 1.06, 1.02; R^2 =.72, .86, .94, .98, and .99). RNIOC for 10yr herd life opportunity estimated from complete lactations was regressed on 5 to 10 yr herd life opportunity based on 305d lactations (β = 1.12, 1.05, 1.01, .97,